

C1

FIG. 11B. Partial nucleotide sequence (SEQ ID NO:26) and deduced amino acid sequence (SEQ ID NO:27) of the maize *SCLm1* gene (Zm-Scl2).

On page 18, line 4, please replace the paragraph beginning "15A-S." with the following paragraph:

C2

FIGS. 15A-S. Comparison of the partial and complete amino acid sequences of several plant members of the *SCARECROW* family of genes. The amino acid sequences are aligned in a manner that maximizes amino acid sequence similarity and identity among *SCR* family members. Each sequence shown is continuous except where noted otherwise; the dots are inserted between two sequence segments in order to align homologous segments. "X" in the middle of a sequence indicates ambiguity in the corresponding nucleotide sequence and, possible termination of the ORF at the "X" residue site. "X" at the end of a sequence indicates termination of the ORF at the "X" residue site. The numbering of the amino acid residues is shown at the bottom of each figure and is based on the Arabidopsis *SCR* amino acid sequence. Conserved Motifs I through VI are indicated by the various dashed lines above the figures. The new and old names of the family members are shown in FIG. 15A. The sequences of *SCR*, Tf1 and Tf4 are of the complete *SCR* protein. The sequence identifier numbers are as follows: *SCR* (SEQ ID NO: 2); 3989 (SEQ ID NO: 36); 12398 (SEQ ID NO: 52); 4871 (SEQ ID NO: 46); 11846 (SEQ ID NO: 59); 2504 (SEQ ID NO: 44); 3935 (SEQ ID NO: 21); 11261 (SEQ ID NO: 50); 713 (SEQ ID NO: 43); 10964 (SEQ ID NO: 48); 23196 (SEQ ID NO: 58); Tf1 (SEQ ID NO: 34); Tf4 (SEQ ID NO: 35); 18310 (SEQ ID NO: 37); 18652 (SEQ ID NO: 54); 4818 (SEQ ID NO: 19); 21729 (SEQ ID NO: 151); 1110 (SEQ ID NO: 23); 174 (SEQ ID NO: 42); and 33/08 (SEQ ID NO: 41).

On page 22, line 3, please replace the paragraph beginning "FIG. 25." with the following paragraph:

C3

FIG25A-B. Maize Scarecrow gene. The nucleotide (SEQ ID NO: 95) and deduced amino acid sequence (SEQ ID NO: 96) of the maize scarecrow gene (*ZCR*) is shown. The amino acid numbers are shown on the right, while the nucleotides are numbered on the left.

On page 22, line 7, please replace the paragraph beginning "FIG. 26." with the following paragraph:

C4

FIG. 26A. Amino acid sequence alignment of maize ZCR (SEQ ID NO: 96) and Arabidopsis SCR (SEQ ID NO: 2). Identical residues are marked by asterisks. In addition, three copies of an LXXLL motif are underlined.

On page 22, line 27, please replace the paragraph beginning "FIG. 28A-AH." with the following paragraph:

C5

FIGS. 28A-AH. The partial nucleotide and amino acid sequences of Arabidopsis EST's that encode members of the SCARECROW-like (SCL) gene family (SEQ ID NOS: 68-94, 23, 21, 19, 46, 50, 54, and 58 respectively). "N" indicates an unknown base.

On page 22, line 33 to page 23, line 8, please replace the paragraph beginning "FIG. 29." with the following paragraph:

C6

FIG. 29. Alignment of the Arabidopsis GRAS gene products (SCL3 (SEQ ID NO: 21), SCL11 (SEQ ID NO: 50), SCL9 (SEQ ID NO: 113), SCL14 (SEQ ID NO: 58), SCL16 (SEQ ID NO: 126), SCL13 (SEQ ID NO: 54), SCL5 (SEQ ID NO: 128), SCL1 (SEQ ID NO: 23), SCL8 (SEQ ID NO: 116), SCL4 (SEQ ID NO: 117), SCL7 (SEQ ID NO: 52), SCL6 (SEQ ID NO: 46; residues 21-378), SCL15 (SEQ ID NO: 119), SCL18 (SEQ ID NO: 120), GAI (SEQ ID NO: 150), RGA (SEQ ID NO: 149), RGAL (SEQ ID NO: 123), SCL 19 (SEQ ID NO: 130 and SCR (SEQ ID NO: 2)). The highly conserved region of the GRAS products can be divided into five recognizable motifs, indicated in the figure. See also, for example, Section 5.1.5., *infra*. The absolutely conserved residues within the VHIID (SEQ ID NO: 145) and SAW (SEQ ID NO: 146) motifs are highlighted in bold, as are the hydrophobic residues of the leucine heptads, the P-F-Y-R-E residues of the PFYRE motif (SEQ ID NO: 147), and the two short sequences that define the end of the VHIID motif (SEQ ID NO: 145) and the beginning of the PFYRE motif (SEQ ID NO: 147). The @ symbol in the alignment indicates the location of an apparent insertion in the SCL3 gene (SEQ ID NO: 148). The deduced amino acid sequence of the insertion is shown at the bottom of the figure.

On page 24, line 1, please replace the paragraph beginning "FIG. 33." with the following paragraph:

C7  
FIG. 33. CBPBTT44 Partial cDNA (SEQ ID NO: 104) and Amino Acid Sequence (SEQ ID NO: 105). The partial nucleotide and amino acid sequence of CBPBTT44, a closely related gene to the maize ZCR gene.

On page 24, line 4, please replace the paragraph beginning "FIG. 34." with the following paragraph:

C8  
FIG. 34. Alignment of the Arabidopsis SCR (SEQ ID NO: 2, positions 364-653), the maize ZCR (SEQ ID NO: 101) and the CBPBTT44 (SEQ ID NO: 102) amino acid sequence. As shown in bold, all three genes contain the leucine heptad repeats. The alignment further shows that all three genes share a high degree of homology.

On page 37, line 10, please replace the section beginning "PRIMERS:" with the following paragraph:

PRIMERS:

**Forward:**

C9  
Name: SCR5AII (23-mer, 2 inosines, 64-mix)  
A.A. code: HFTANQAI (SEQ ID NO: 134)  
DNA Sequence: 5' CAT/C TTT/C ACI GCI AAT/C CAA/G GCN AT 3'  
(SEQ ID NO: 133)

Name: SCR5B (29-mer, 1 inosine, 144-mix)  
A.A. code: VHIID(L/F)D (SEQ ID NO: 136)  
DNA Sequence: 5' ACGTCTCGA GTI CAT/C ATA/C/T ATA/C/T GAT/C  
TTN GA 3' (SEQ ID NO: 135)